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The Genetic Mechanism of Resistance to Antibiotics in Bacillus pumilus 3-19 Strain

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Abstract

© 2016, Springer Science+Business Media New York.Treatment of bacterial infections becomes increasingly complicated due to the emergence of bacterial resistance to antimicrobial agents. Until now, most studies on bacterial antibiotic resistance have focused mainly on clinically relevant isolates pathogenic microorganisms and lactic acid bacteria. Very limited information on the antimicrobial susceptibility profiles of Bacillus spp. is available. In this paper, we used Bacillus pumilus 3-19 strain, a derivative of a wild B. pumilus 7P strain that has acquired resistance to streptomycin. Comparative analysis of genomes showed that B. pumilus 3-19 became resistant to streptomycine due to a mutation in 56 codon of the rpsL gene (S12 protein of 30S ribosomal subunit) that resulted in the replacement of lysine with asparagine in the binding site of streptomycin. Bioinformatic analysis of rpoB gene (β-subunit of RNA polymerase) showed that there is also a point mutation in 185 codon, which can lead to rifampicin resistance. Nevertheless, B. pumilus 3-19 strain remained sensitive to rifampicin in disc diffusion assay.

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Keywords

Antibiotic, Bacillus pumilus, Genome analysis, Resistance

References

[1] Chudobova, D., Dostalova, S., Blazkova, I., et al. (2014). Effect of ampicillin, streptomycin, penicillin and tetracycline on metal resistant and non-resistant Staphylococcus aureus. International Journal of Environmental Research and Public Health, 11, 3233–3255.

[2] Gatica, J., & Cytryn, E. (2013). Impact of treated wastewater irrigation on antibiotic resistance in the soil microbiome. Environmental Science and Pollution Research International, 20, 3529–3538.

[3] Wright, G. D. (2003). Mechanisms of resistance to antibiotics. Current Opinion in Chemical Biology, 7, 563–569.

[4] Tenover, F. C. (2006). Mechanisms of antimicrobial resistance in bacteria. American Journal of Infection Control, 34, 3–10.

[5] Mingeot-Leclercq, M. P., Glupczynski, Y., Tulkens, P. M. (1999). Aminoglycosides: activity and resistance. Antimicrobial Agents and Chemotherapy, 43, 727–737.

[6] McManus, M. C. (1997). Mechanisms of bacterial resistance to antimicrobial agents. American Journal of Health-System Pharmacy, 54, 1420–1433.

[7] Carter, A. P., Clemons, W. M., Brodersen, D. E., Morgan-Warren, R. J., Wimberly, B. T., Ramakrishnan, V. (2000). Functional insights from the structure of the 30S ribosomal subunit and its interactions with antibiotics. Nature, 407, 340–348.

[8] Inaoka, T., Kasai, K., Ochi, K. (2001). Construction of an in vivo nonsense readthrough assay system and functional analysis of ribosomal proteins S12, S4, and S5 in Bacillus subtilis. Journal of Bacteriology, 183, 4958–4963.

[9] Garcia-Ramon, D. C., Molina, C. A., Osuna, V. S. (2016). An in-depth characterization of the entomopathogenic strain Bacillus pumilus 15.1 reveals that it produces inclusion bodies similar to the parasporal crystals of Bacillus thuringiensis. Applied Microbiology and Biotechnology, 100(8), 3637–3654. doi:10.1007/s00253-01--7259-9.

[10] Padaria, J. C., Sarkar, K., Lone, S. A., Srivastava, S. (2014). Molecular characterization of cellulose-degrading Bacillus pumilus from the soil of tea garden, Darjeeling hills, India. Journal of Environmental Biology, 35, 555–561.

[11] Sharipova, M. R., Balaban, N. P., Kayumov, A. R., et al. (2008). The expression of the serine proteinase gene of Bacillus intermedius in Bacillus subtilis. Microbiological Research, 163, 39–50.

[12] Danilova, Y. V., Shagimardanova, E. I., Margulis, A. B. (2014). Bacterial enzymes effectively digest Alzheimer's β-amyloid peptide. Brain Research Bulletin, 108, 113–117. doi:10.1016/j.brainresbull.2014.08.009.

[13] Shagimardanova EI, Toymentseva AA, Balaban NP et al (2014) Draft genome sequence of Bacillus pumilus 7P, isolated from the soil of the Tatarstan Republic, Russia. Genome Announc. doi:10.1128/genomeA.00599-14.

[14] Ulyanova V, Shah Mahmud R, Dudkina E, Vershinina V, Ilinskaya O (2014) Draft Whole Genome Sequence of Bacillus pumilus Strain 3-19, a Chemical Mutant Overproducing Extracellular Ribonuclease. Genome Announc. 24;2(4). doi: 10.1128/genomeA.00724-14.

[15] Sambrook, J., Fritsch, E. F., Maniatis, T. (1989). Molecular cloning: a laboratory manual (Cold Spring Harbor Laboratory Press 2nd ed.). New York: Cold Spring Harbor.

[16] Sun, Y., Duan, X., Wang, L., Wu, J. (2016). Enhanced maltose production through mutagenesis of acceptorbinding subsite +2 in Bacillus stearothermophilus maltogenic amylase. Journal of Biotechnology, 217, 53–61.

[17] Okamoto-Hosoya, Y., Hosaka, T., Ochi, K. (2003). An aberrant protein synthesis activity is linked with antibiotic verproduction in rpsL mutants of Streptomyces coelicolor A3 (2). Microbiology, 149, 3299–3309.

[18] Sharipova, M. R., Balaban, N. P., Leschinskaya, I. B. (1994). Production of extracellular alkaline phosphatase by Bacillus pumilus antibiotic resistant strains. Microbiology, 63, 52–58.

[19] Kurosawa, K., Hosaka, T., Tamehiro, N., Inaoka, T., Ochi, K. (2006). Improvement of α-amylase production by modulation of ribosomal component protein S12 in Bacillus subtilis 168. Applied and Environmental Microbiology, 72(1), 71–77.

[20] Nicholson WL, Park R. (2015) Anaerobic growth of Bacillus subtilis alters the spectrum of spontaneous mutations in the rpoB gene leading to rifampicin resistance. FEMS Microbiol Lett 362(24):fnv213. doi: 10.1093/femsle/fnv213.